



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/788,746

DATE: 09/01/2004

TIME: 11:45:34

Input Set : N:\Crif3\RULE60\10788746.raw

Output Set: N:\CRF4\09012004\J788746.raw

1 <110> APPLICANT: Akzo Nobel NV  
 2 <120> TITLE OF INVENTION: Structural Proteins of Fish Pancreatic Disease Virus  
 3 and Uses Thereof  
 4 <130> FILE REFERENCE: I/98376US  
 5 <140> CURRENT APPLICATION NUMBER: US/10/788,746  
 6 <141> CURRENT FILING DATE: 2004-02-26  
 7 <150> PRIOR APPLICATION NUMBER: US/09/674,866  
 8 <151> PRIOR FILING DATE: 2001-06-04  
 9 <150> PRIOR APPLICATION NUMBER: EP98201461.5  
 10 <151> PRIOR FILING DATE: 1998-05-08  
 11 <160> NUMBER OF SEQ ID NOS: 15  
 12 <170> SOFTWARE: PatentIn Ver. 2.1  
 14 <210> SEQ ID NO: 1  
 15 <211> LENGTH: 5179  
 16 <212> TYPE: DNA  
 17 <213> ORGANISM: Salmon pancreatic disease virus  
 18 <400> SEQUENCE: 1

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21	gtatgtcttt	catctacaag	gggccaaggc	caatgtgatg	cacagcagag	tcgaagccgt	180
22	atgccctgac	ctctcggagg	tggctatgga	caggttcaca	ctagacatga	aacgcgacgt	240
23	caaagtgcag	ccaggcacga	agcacgtaga	ggagagacct	aaagtccaag	agattcaagc	300
24	ggccgacccc	atggccaccg	cgtacttggtg	cgccatccat	agagagctag	tccgaaggct	360
25	gaaggccgtc	ctgaaaccgt	ctatacacgt	gttgttcgat	atgagctccg	aggattttga	420
26	tgctatcgtg	ggccatggga	tgaagttggg	tgacaagggtg	ctggaaacgg	acatctcctc	480
27	attcgacaag	agccaggacc	aagccatggc	ggttacagcg	ctgatgctgc	tgagggactt	540
28	gggagtagaa	gaagacctcc	tgaccctaata	tgaggcgtct	ttcggcgaca	tcacttctgc	600
29	ccacctgccc	acaggcacca	gatttcagtt	tggatcgatg	atgaagtctg	gactttttct	660
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33	ggacatggaa	attggcaaca	tgagtcctta	tttttggggc	ggcttcctgt	tactcgacac	900
34	ggtaacaggc	actgtaagcc	gagtgtcgga	ccctgtaaaa	cgctgatga	agatgggaaa	960
35	accggccctg	aacgatccag	aaacggacgt	ggacagatgc	cgcgactgc	gcgaagaagt	1020
36	ggaaagctgg	tacagagtgg	ggattcagtg	gccactgcag	gtggctgccg	ccacacgcta	1080
37	tggcgtgaac	cacctgccgc	tggccacaat	ggcgatggcc	acgctcgccc	aggacttgag	1140
38	atcgtaacctg	ggcgcgcgag	gggagtacgt	atccctctac	gtctaacctt	aatattttct	1200
39	gcatcatact	tccaaacaat	catgtttccc	atgcaattca	ccaactcagc	ctatcgccag	1260
40	atggagccca	tgtttgcacc	gggttccccga	ggacaagtac	agccgtaccg	gccgcgcact	1320
41	aagcgccgcc	aggagccgca	agtcgggaac	gccgccatta	ctgccctcgc	gaaccagatg	1380
42	agtgcgtccc	agttgcaggt	agctggactt	gccggccagg	caaggggtga	ccgccgtggg	1440
43	ccaagacgtg	ttcagaagaa	caagcagaag	aagaagaact	cttccaacgg	agaaaaaccc	1500
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46 agcaccttcc ccgtgtacca cgaagggtgct atatccggct acgctgtgct gattggatct 1680
47 cgcgtattca agccggcaca cgtgaagggt aagatcgacc accctgaact ggcagacatc 1740
48 aagttccagg tcgccgagga catggacctc gaagcagctg cgtacccgaa gagcatgcga 1800
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94      gcaccgcacg gttgtaagat cagtgccaat ccgctcctgg ccctcgattg tgggggttgg 4560
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96      aaaccatcgg ccctgaaatg cgtggtggac agctgcgagt acggggtgga ctacgggggc 4680
97      gccgccacga tcacctacga gggccacgag gccgggaagt gcgggattca ttccctgaca 4740
98      ccaggagtcc ccctgagaac atcggtggtt gaagtggttg ctggcgccaa taccgtcaaa 4800
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103     tgccgctcca aaagaatccg gatagtcaag agctaaattc cggatacaca attgctcact 5100
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105     atacaaaaaa aaaaaaaaaa                                     5179
107 <210> SEQ ID NO: 2
108 <211> LENGTH: 394
109 <212> TYPE: PRT
110 <213> ORGANISM: Salmon pancreatic disease virus
111 <220> FEATURE:
112 <223> OTHER INFORMATION: NSP4 (C-terminal region)
113 <400> SEQUENCE: 2
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117         20             25             30
118     Leu Ser Pro Gly Gln Ile Glu Glu Tyr Val Phe His Leu Gln Gly Ala
119         35             40             45
120     Lys Ala Asn Val Met His Ser Arg Val Glu Ala Val Cys Pro Asp Leu
121         50             55             60
122     Ser Glu Val Ala Met Asp Arg Phe Thr Leu Asp Met Lys Arg Asp Val
123         65             70             75             80
124     Lys Val Thr Pro Gly Thr Lys His Val Glu Glu Arg Pro Lys Val Gln
125         85             90             95
126     Glu Ile Gln Ala Ala Asp Pro Met Ala Thr Ala Tyr Leu Cys Ala Ile
127         100            105            110
128     His Arg Glu Leu Val Arg Arg Leu Lys Ala Val Leu Lys Pro Ser Ile
129         115            120            125
130     His Val Leu Phe Asp Met Ser Ser Glu Asp Phe Asp Ala Ile Val Gly
131         130            135            140
132     His Gly Met Lys Leu Gly Asp Lys Val Leu Glu Thr Asp Ile Ser Ser
133         145            150            155            160
134     Phe Asp Lys Ser Gln Asp Gln Ala Met Ala Val Thr Ala Leu Met Leu
135         165            170            175
136     Leu Arg Asp Leu Gly Val Glu Glu Asp Leu Leu Thr Leu Ile Glu Ala
137         180            185            190
138     Ser Phe Gly Asp Ile Thr Ser Ala His Leu Pro Thr Gly Thr Arg Phe
139         195            200            205
140     Gln Phe Gly Ser Met Met Lys Ser Gly Leu Phe Leu Thr Leu Phe Val
141         210            215            220
142     Asn Thr Leu Leu Asn Ile Thr Ile Ala Ala Arg Val Leu Arg Glu Gln
143         225            230            235            240

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146      Thr Gly Val Val Ser Asp Asp Met Met Val Ala Arg Cys Ala Ser Trp
147              260              265              270
148      Leu Asn Met Glu Val Lys Ile Met Asp Met Glu Ile Gly Asn Met Ser
149              275              280              285
150      Pro Tyr Phe Cys Gly Gly Phe Leu Leu Leu Asp Thr Val Thr Gly Thr
151              290              295              300
152      Val Ser Arg Val Ser Asp Pro Val Lys Arg Leu Met Lys Met Gly Lys
153      305              310              315              320
154      Pro Ala Leu Asn Asp Pro Glu Thr Asp Val Asp Arg Cys Arg Ala Leu
155              325              330              335
156      Arg Glu Glu Val Glu Ser Trp Tyr Arg Val Gly Ile Gln Trp Pro Leu
157              340              345              350
158      Gln Val Ala Ala Ala Thr Arg Tyr Gly Val Asn His Leu Pro Leu Ala
159              355              360              365
160      Thr Met Ala Met Ala Thr Leu Ala Gln Asp Leu Arg Ser Tyr Leu Gly
161      370              375              380
162      Ala Arg Gly Glu Tyr Val Ser Leu Tyr Val
163      385              390
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 1359
167 <212> TYPE: PRT
168 <213> ORGANISM: Salmon pancreatic disease virus
169 <220> FEATURE:
170 <223> OTHER INFORMATION: p130
171 <400> SEQUENCE: 3
172      Met Pro Arg Thr Ala Arg Arg Ser Gly Lys Leu Val Gln Ser Gly Asp
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175              20              25              30
176      Pro Ala Ala Gly His Asn Gly Asp Gly His Ala Arg Pro Gly Leu Glu
177      35              40              45
178      Ile Val Pro Gly Arg Ala Arg Gly Val Arg Ile Pro Leu Arg Leu Thr
179      50              55              60
180      Leu Ile Phe Ser Ala Ser Tyr Phe Gln Thr Ile Met Phe Pro Met Gln
181      65              70              75              80
182      Phe Thr Asn Ser Ala Tyr Arg Gln Met Glu Pro Met Phe Ala Pro Gly
183              85              90              95
184      Ser Arg Gly Gln Val Gln Pro Tyr Arg Pro Arg Thr Lys Arg Arg Gln
185              100              105              110
186      Glu Pro Gln Val Gly Asn Ala Ala Ile Thr Ala Leu Ala Asn Gln Met
187      115              120              125
188      Ser Ala Leu Gln Leu Gln Val Ala Gly Leu Ala Gly Gln Ala Arg Val
189      130              135              140
190      Asp Arg Arg Gly Pro Arg Arg Val Gln Lys Asn Lys Gln Lys Lys Lys
191      145              150              155              160
192      Asn Ser Ser Asn Gly Glu Lys Pro Lys Glu Lys Lys Lys Lys Gln Lys
193              165              170              175

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195				180					185					190		
196	Asn	Arg	Pro	Gly	Lys	Glu	Val	Arg	Ile	Ser	Val	Lys	Cys	Ala	Arg	Gln
197			195					200					205			
198	Ser	Thr	Phe	Pro	Val	Tyr	His	Glu	Gly	Ala	Ile	Ser	Gly	Tyr	Ala	Val
199		210					215					220				
200	Leu	Ile	Gly	Ser	Arg	Val	Phe	Lys	Pro	Ala	His	Val	Lys	Gly	Lys	Ile
201		225				230					235					240
202	Asp	His	Pro	Glu	Leu	Ala	Asp	Ile	Lys	Phe	Gln	Val	Ala	Glu	Asp	Met
203				245						250					255	
204	Asp	Leu	Glu	Ala	Ala	Ala	Tyr	Pro	Lys	Ser	Met	Arg	Asp	Gln	Ala	Ala
205			260						265					270		
206	Glu	Pro	Ala	Thr	Met	Met	Asp	Arg	Val	Tyr	Asn	Trp	Glu	Tyr	Gly	Thr
207			275					280					285			
208	Ile	Arg	Val	Glu	Asp	Asn	Val	Ile	Ile	Asp	Ala	Ser	Gly	Arg	Gly	Lys
209		290				295						300				
210	Pro	Gly	Asp	Ser	Gly	Arg	Ala	Ile	Thr	Asp	Asn	Ser	Gly	Lys	Val	Val
211		305				310					315					320
212	Gly	Ile	Val	Leu	Gly	Gly	Gly	Pro	Asp	Gly	Arg	Arg	Thr	Arg	Leu	Ser
213				325						330					335	
214	Val	Ile	Gly	Phe	Asp	Lys	Lys	Met	Lys	Ala	Arg	Glu	Ile	Ala	Tyr	Ser
215			340						345					350		
216	Asp	Ala	Ile	Pro	Trp	Thr	Arg	Ala	Pro	Ala	Leu	Leu	Leu	Leu	Pro	Met
217		355						360					365			
218	Val	Ile	Val	Cys	Thr	Tyr	Asn	Ser	Asn	Thr	Phe	Asp	Cys	Ser	Lys	Pro
219		370					375					380				
220	Ser	Cys	Gln	Asp	Cys	Cys	Ile	Thr	Ala	Glu	Pro	Glu	Lys	Ala	Met	Thr
221		385				390					395					400
222	Met	Leu	Lys	Asp	Asn	Leu	Asn	Asp	Pro	Asn	Tyr	Trp	Asp	Leu	Leu	Ile
223				405						410					415	
224	Ala	Val	Thr	Thr	Cys	Gly	Ser	Ala	Arg	Arg	Lys	Arg	Ala	Val	Ser	Thr
225			420						425					430		
226	Ser	Pro	Ala	Ala	Phe	Tyr	Asp	Thr	Gln	Ile	Leu	Ala	Ala	His	Ala	Ala
227		435						440					445			
228	Ala	Ser	Pro	Tyr	Arg	Ala	Tyr	Cys	Pro	Asp	Cys	Asp	Gly	Thr	Ala	Cys
229		450					455					460				
230	Ile	Ser	Pro	Ile	Ala	Ile	Asp	Glu	Val	Val	Ser	Ser	Gly	Ser	Asp	His
231		465				470					475					480
232	Val	Leu	Arg	Met	Arg	Val	Gly	Ser	Gln	Ser	Gly	Val	Thr	Ala	Lys	Gly
233				485						490					495	
234	Gly	Ala	Ala	Gly	Glu	Thr	Ser	Leu	Arg	Tyr	Leu	Gly	Arg	Asp	Gly	Lys
235			500						505					510		
236	Val	His	Ala	Ala	Asp	Asn	Thr	Arg	Leu	Val	Val	Arg	Thr	Thr	Ala	Lys
237		515						520					525			
238	Cys	Asp	Val	Leu	Gln	Ala	Thr	Gly	His	Tyr	Ile	Leu	Ala	Asn	Cys	Pro
239		530					535					540				
240	Val	Gly	Gln	Ser	Leu	Thr	Val	Ala	Ala	Thr	Leu	Asp	Gly	Thr	Arg	His
241		545				550					555					560
242	Gln	Cys	Thr	Thr	Val	Phe	Glu	His	Gln	Val	Thr	Glu	Lys	Phe	Thr	Arg

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L:5 M:270 C: Current Application Number differs, Replaced Current Application Number